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<110> Bintrim, Scott
 Bevan, Scott
 Zhu, Baolong
 Merlo, Donald J.

<120> Pesticidally Active Proteins and Polynucleotides Obtainable from
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 <151> 2002-06-28

<150> US 60/441,647
 <151> 2003-01-21

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Val Ala Gln Leu Tyr Arg Leu Gly Arg Ile Pro His Met Leu Gly Leu
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Arg Phe Thr Glu Ala Glu Leu Leu Trp Lys Leu Met Ala Gly Gly Glu
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Asp Thr Leu Leu Arg Thr Ile Gly Ala Lys Pro Arg Ser Leu Gln Ala
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Leu Glu Ile Ile Arg Arg Thr Glu Val Leu Leu Asp Trp Met Asp Ala
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His Gln Leu Asp Val Val Ser Leu Gln Ala Met Val Thr Asn Arg Tyr

[illegible]

Glu Ser Trp Val Asn Leu Gly Arg Gln Leu Asn Val Gly Ser Arg
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Thr Leu Gly Glu Leu Val Asp Met Ser Glu Glu Asp Asp Thr Ala
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Glu Asn Thr Asp Leu Ile Ile Ser Val Ala Gln Ser Leu Met Ala
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<212> PRT
<213> Paenibacillus strain IDAS 1529
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Leu Ile Lys Glu Ser Arg Arg Asp Ala Leu Val Asn His Tyr Ile Ala
20          25          30

Asn Asn Val Pro Arg Glu Leu Thr Asp Lys Ile Thr Asp Ala Asp Ser
35          40          45

Leu Tyr Glu Tyr Leu Leu Leu Asp Thr Lys Ile Ser Glu Leu Val Lys
50          55          60

Thr Ser Pro Ile Ala Glu Ala Ile Ser Ser Val Gln Leu Tyr Met Asn
65          70          75          80

Arg Cys Val Glu Gly Tyr Glu Gly Lys Leu Thr Pro Glu Gly Asn Ser
85          90          95

His Phe Gly Pro Gly Lys Phe Leu Asn Asn Trp Asp Thr Tyr Asn Lys

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Arg Tyr Ser Thr Trp Ala Gly Lys Glu Arg Leu Lys Tyr Tyr Ala Gly		
115	120	125
Ser Tyr Ile Asp Pro Ser Leu Arg Tyr Asn Lys Thr Asp Pro Phe Leu		
130	135	140
Asn Leu Glu Gln Asn Ile Ser Gln Gly Arg Ile Thr Asp Asp Thr Val		
145	150	155
Lys Asn Ala Leu Gln His Tyr Leu Thr Glu Tyr Glu Val Leu Ala Asp		
	165	170
Leu Glu Tyr Ile Ser Val Asn Lys Gly Ala Asp Glu Ser Val Leu Phe		
	180	185
Phe Val Gly Arg Thr Lys Thr Met Pro Tyr Glu Tyr Tyr Trp Arg Arg		
	195	200
Leu Thr Leu Lys Lys Asp Asn Asn Asn Lys Leu Val Pro Ala Ile Trp		
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Ser Gln Trp Lys Lys Ile Thr Ala Asn Ile Gly Glu Ala Val Asn Asn		
225	230	235
Tyr Val Val Leu His Trp His Asn Asn Arg Leu His Val Gln Trp Gly		
	245	250
Ser Thr Glu Lys Thr Gln Asn Asp Asp Gly Glu Pro Ile Glu Lys Arg		
	260	265
Tyr Leu Asn Asp Trp Phe Met Asp Lys Ser Ser Val Trp Ser Ser Phe		
	275	280
Arg Lys Val Ser Tyr Ile Glu Asn Ser Phe Thr Tyr Thr Glu Gly Ile		
	290	295
Ile Asp Ser Arg Asn Ile Thr Ile Ala Gly Asn Gln Leu Phe Cys Asp		
305	310	315
Asp Ser Asn Thr Phe Lys Ala Thr Ile Thr Ala Leu Pro Phe Asp Gln		
	325	330
		335

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Ile Arg Val Tyr Leu Glu Lys Ile Tyr Gly Thr Gly Gly Ser Ile Thr
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Val Thr Gly Glu Asn Lys Gly Tyr Ile Ile Lys Val Gly Glu Pro Arg
      355                      360                      365

Glu Val Ser Phe Ser Pro Asn Thr Leu Leu Asp Val Phe Ile Gly Ser
      370                      375                      380

Asn Ala Ser Pro Arg Asp Pro Tyr Phe Lys Ala Thr Phe Asn Arg Glu
      385                      390                      395                      400

Ala Leu Gln Asn Ser Tyr Gly Ser Ile Lys Ile Asn Gln Tyr Thr Pro
      405                      410                      415

Pro Ser Gly Ser Asn Ile Lys Gly Pro Ile Asp Leu Thr Leu Lys Asn
      420                      425                      430

Asn Ile Asp Leu Ser Ala Leu Leu Glu Glu Ser Leu Asp Val Leu Phe
      435                      440                      445

Asp Tyr Thr Ile Gln Gly Asn Asn Gln Leu Gly Gly Leu Glu Ala Phe
      450                      455                      460

Asn Gly Pro Tyr Gly Leu Tyr Leu Trp Glu Ile Phe Leu His Val Pro
      465                      470                      475                      480

Phe Leu Met Ala Val Arg Phe His Thr Glu Gln Arg Tyr Glu Leu Ala
      485                      490                      495

Glu Arg Trp Phe Lys Phe Ile Phe Asn Ser Ala Gly Tyr Arg Asp Gly
      500                      505                      510

Tyr Gly Asn Leu Leu Thr Asp Asp Lys Gly Asn Val Arg Tyr Trp Asn
      515                      520                      525

Val Val Pro Leu Gln Glu Asp Thr Glu Trp Asp Asp Thr Leu Ser Leu
      530                      535                      540

Ala Thr Thr Asp Pro Asp Glu Ile Ala Met Ala Asp Pro Met Gln Tyr
      545                      550                      555                      560

Lys Leu Ala Ile Phe Ile His Thr Leu Asp Phe Leu Ile Ser Arg Gly
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Asp Ser Leu Tyr Arg Met Leu Glu Arg Asp Thr Leu Thr Glu Ala Lys
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Met Tyr Tyr Ile Gln Ala Ser Gln Leu Leu Gly Pro Arg Pro Glu Ile
 595 600 605

Arg Ile Asn His Ser Trp Pro Asp Pro Thr Leu Gln Ser Glu Ala Asp
 610 615 620

Ala Val Thr Ala Val Pro Thr Arg Ser Asp Ser Pro Ala Ala Pro Ile
 625 630 635 640

Leu Ala Leu Arg Ala Leu Leu Asn Ala Glu Asn Gly His Phe Leu Pro
 645 650 655

Pro Tyr Asn Asp Glu Leu Leu Ala Phe Trp Asp Lys Ile Asp Leu Arg
 660 665 670

Leu Tyr Asn Leu Arg His Asn Leu Ser Leu Asp Gly Gln Pro Leu His
 675 680 685

Leu Pro Leu Phe Thr Glu Pro Val Asn Pro Arg Glu Leu Gln Val Gln
 690 695 700

His Gly Ala Gly Asp Gly Leu Gly Gly Ser Ala Gly Ser Val Gln Ser
 705 710 715 720

Arg Gln Ser Val Tyr Arg Phe Pro Leu Val Ile Asp Lys Ala Arg Asn
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Ala Ala Ser Ser Val Ile Gln Phe Gly Asn Ala Leu Glu Asn Ala Leu
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Thr Lys Gln Asp Ser Glu Ala Met Thr Met Leu Leu Gln Ser Gln Gln
 755 760 765

Gln Ile Val Leu Gln Gln Thr Arg Asp Ile Gln Glu Lys Asn Leu Ala
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Ser Leu Gln Ala Ser Leu Glu Ala Thr Met Thr Ala Lys Ala Gly Ala
 785 790 795 800

Lys Ser Arg Lys Thr His Phe Ala Gly Leu Ala Asp Asn Trp Met Ser
 805 810 815

His Asn Glu Thr Ala Ser Leu Ala Leu Arg Thr Thr Ala Gly Ile Ile
 820 825 830

Asn Thr Ser Ser Thr Val Pro Ile Ala Ile Thr Gly Gly Leu Asp Met
 835 840 845

Ala Pro Asn Ile Phe Gly Phe Ala Val Gly Gly Ser Arg Trp Gly Ala
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Ala Ser Ala Ala Val Ala Gln Gly Leu Gln Ile Ala Ala Gly Val Met
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Glu Gln Thr Ala Asn Ile Ile Asp Ile Ser Glu Ser Tyr Arg Arg Arg
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Arg Glu Asp Trp Leu Leu Gln Arg Asp Val Ala Glu Asn Glu Ala Ala
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Gln Leu Asp Ser Gln Ile Ala Ala Leu Arg Glu Gln Met Asp Met Ala
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Arg Lys Gln Leu Ala Leu Ala Glu Thr Glu Gln Ala His Ala Gln Ala
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Val Tyr Glu Leu Leu Ser Thr Arg Phe Thr Asn Gln Ala Leu Tyr Asn
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Trp Met Ala Gly Arg Leu Ser Ser Leu Tyr Tyr Gln Met Tyr Asp Ala
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Ala Leu Pro Leu Cys Leu Met Ala Lys Gln Ala Leu Glu Lys Glu Ile
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Gly Asn Asp Lys Thr Val Gly Ile Phe Thr Leu Pro Ala Trp Asn Asp
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Leu Tyr Gln Gly Leu Leu Ala Gly Glu Ala Leu Leu Leu Glu Leu
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Gln Lys Leu Glu Asn Leu Trp Leu Glu Glu Asp Lys Arg Gly Met
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Glu Ala Val Arg Thr Val Ser Leu Asp Thr Leu Leu Arg Lys Glu

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 Gly Lys Thr Pro Asp Pro Val Ser Gly Val Ser Val Gln Leu Gln
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 Asn Asn Ile Phe Ser Ala Thr Leu Asp Leu Ser Thr Leu Gly Leu
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 Asp Arg Phe Tyr Asn Gln Ala Glu Lys Ala His Arg Ile Lys Asn
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 Leu Ser Val Thr Leu Pro Ala Leu Leu Gly Pro Tyr Gln Asp Ile
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 Ala Ala Thr Leu Ser Leu Gly Gly Glu Thr Val Ala Leu Ser His
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 Gly Val Asp Asp Ser Gly Leu Phe Ile Thr Asp Leu Asn Asp Ser
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 Arg Phe Leu Pro Phe Glu Gly Met Asp Pro Leu Ser Gly Thr Leu
 1160 1165 1170
 Val Leu Ser Ile Leu His Ala Gly Gln Asp Gly Asp Gln Arg Leu
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 Met Lys
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<211> 1099

<212> PRT

<213> Paenibacillus strain IDAS 1529

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Glu Glu Leu Thr Glu Ala Leu Lys Gln Ser Gly Tyr Arg Thr Val Phe
20           25           30

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Asp Ile Val Ser Asp Asn Leu Ala Glu Phe Gln Lys Asn Asn Pro Glu
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Ile Pro Ser Ser Asp Ala Lys Glu Ile His Gln Leu Ala Val Gln Arg
 50 55 60

Thr Glu Asn Leu Cys Met Leu Tyr Lys Ala Trp Gln Leu His Asn Asp
 65 70 75 80

Pro Val Val Gln Ser Leu Pro Lys Leu Ser Ala Asp Thr Gly Leu Gln
 85 90 95

Gly Met Arg Ala Ala Leu Glu Arg Ser Leu Gly Gly Gly Ala Asp Phe
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Gly Asp Leu Phe Pro Glu Arg Ser Pro Glu Gly Tyr Ala Glu Ala Ser
 115 120 125

Ser Ile Gln Ser Leu Phe Ser Pro Gly Arg Tyr Leu Thr Val Leu Tyr
 130 135 140

Lys Ile Ala Arg Asp Leu His Asp Pro Lys Asp Lys Leu His Ile Asp
 145 150 155 160

Asn Arg Arg Pro Asp Leu Lys Ser Leu Ile Leu Asn Asn Asp Asn Met
 165 170 175

Asn Arg Glu Val Ser Ser Leu Asp Ile Leu Leu Asp Val Leu Gln Pro
 180 185 190

Glu Gly Ser Asp Thr Leu Thr Ser Leu Lys Asp Thr Tyr His Pro Met
 195 200 205

Thr Leu Pro Tyr Asp Asp Asp Leu Ala Gln Ile Asn Ala Val Ala Glu
 210 215 220

Ala Arg Ser Ser Asn Leu Leu Gly Ile Trp Asp Thr Leu Leu Asp Thr
 225 230 235 240

Gln Arg Thr Ser Ile Leu Gln Asn Ser Ala Ala Ala Arg Arg Ile Ser
 245 250 255

Lys Ala Arg His Ser Ala Tyr Ala Asn Gln Lys Ala Ser Asn Asp Glu

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290	295	300
Lys Ile Asn Ile Gly Pro Pro Gln Ala Ala Asp Ile Ala Pro Ala Lys		
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Arg Val Ala Asp Asp Val Ser Leu Gly Gly Lys Leu Leu Thr Asn Cys		
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Tyr Leu Thr Ser Asp Asp Gly Gln Ser Asn Asn Ile Ser Gly Pro Tyr		
	355	360
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Cys Leu Met Ile Asn Arg Gly Thr Gly Ser Met Pro Ser Gly Thr His		
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Leu Pro Val Gln Ile Glu Arg Val Thr Asp Thr Ser Ile Arg Ile Phe		
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Val Pro Asp His Gly Tyr Leu Gly Leu Gly Glu Ser Leu Ala Ser Asn		
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Trp Asn Glu Pro Leu Ala Leu Asn Leu Gly Leu Asp Glu Ala Leu Thr		
	420	425
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Phe Thr Leu Arg Lys Lys Glu Thr Gly Asn Asp Thr Ile Ser Ile Ile		
	435	440
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Asp Met Leu Pro Pro Val Ala Asn Thr Thr Pro Ser Pro Pro Thr Arg		
	450	455
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Glu Thr Leu Ser Leu Thr Pro Asn Ser Phe Arg Leu Leu Val Asn Pro		
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Glu Pro Thr Ala Glu Asp Ile Ala Lys His Tyr Asn Val Thr Thr Val		
	485	490
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Thr Arg Ala Pro Ala Asp Leu Ala Ser Ala Leu Asn Val Val Asp Asp
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Phe Cys Leu Lys Thr Gly Leu Ser Phe Asn Glu Leu Leu Asp Leu Thr
      515                      520                      525

Met Gln Lys Asp Tyr Gln Ser Lys Ser Ser Glu Tyr Lys Ser Arg Phe
      530                      535                      540

Val Lys Phe Gly Gly Gly Glu Asn Val Pro Val Ser Ser Tyr Gly Ala
      545                      550                      555                      560

Ala Phe Leu Thr Gly Ala Glu Asp Thr Pro Leu Trp Val Lys Gln Tyr
      565                      570                      575

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Gly Val Thr Ala Asp Glu Phe Ser Arg Ile Gly Lys Tyr Cys Phe Gly
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<210> 11
<211> 1444
<212> PRT
<213> Paenibacillus strain IDAS 1529

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<400> 11
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Pro Lys Gly Gly Gly Ser Met Lys Gly Ile Glu Glu Asn Ile Ala Ala
20           25           30

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Pro Gly Ser Asp Gly Met Ala Arg Cys Asn Val Pro Leu Pro Val Thr
 35 40 45

Ser Gly Arg Tyr Ile Thr Pro Asp Ile Ser Leu Ser Tyr Ala Ser Gly
 50 55 60

His Gly Asn Gly Ala Tyr Gly Met Gly Trp Thr Met Gly Val Met Ser
 65 70 75 80

Ile Ser Arg Arg Thr Ser Arg Gly Thr Pro Ser Tyr Thr Ser Glu Asp
 85 90 95

Gln Phe Leu Gly Pro Asp Gly Glu Val Leu Val Pro Glu Ser Asn Glu
 100 105 110

Gln Gly Glu Ile Ile Thr Arg His Thr Asp Thr Ala Gln Gly Ile Pro
 115 120 125

Leu Gly Glu Thr Phe Thr Val Thr Arg Tyr Phe Pro Arg Ile Glu Ser
 130 135 140

Ala Phe His Leu Leu Glu Tyr Trp Glu Ala Gln Ala Gly Ser Ala Thr
 145 150 155 160

Ala Ser Phe Trp Leu Ile His Ser Ala Asp Gly Val Leu His Cys Leu
 165 170 175

Gly Lys Thr Ala Gln Ala Arg Ile Ala Ala Pro Asp Asp Ser Ala Lys
 180 185 190

Ile Ala Glu Trp Leu Val Glu Glu Ser Val Ser Pro Phe Gly Glu His
 195 200 205

Ile Tyr Tyr Gln Tyr Lys Glu Glu Asp Asn Gln Gly Val Asn Leu Glu
 210 215 220

Glu Asp Asn His Gln Tyr Gly Ala Asn Arg Tyr Leu Lys Ser Ile Arg
 225 230 235 240

Tyr Gly Asn Lys Val Ala Ser Pro Ser Leu Tyr Val Trp Lys Gly Glu
 245 250 255

Ile Pro Ala Asp Gly Gln Trp Leu Tyr Ser Val Ile Leu Asp Tyr Gly
 260 265 270

Glu Asn Asp Thr Ser Ala Asp Val Pro Pro Leu Tyr Thr Pro Gln Gly
 275 280 285

Glu Trp Leu Val Arg Pro Asp Arg Phe Ser Arg Tyr Asp Tyr Gly Phe
 290 295 300

Glu Val Arg Thr Cys Arg Leu Cys Arg Gln Val Leu Met Phe His Val
 305 310 315 320

Phe Lys Glu Leu Gly Gly Glu Pro Ala Leu Val Trp Arg Met Gln Leu
 325 330 335

Glu Tyr Asp Glu Asn Pro Ala Ala Ser Met Leu Ser Ala Val Arg Gln
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Leu Ala Tyr Glu Ala Asp Gly Ala Ile Arg Ser Leu Pro Pro Leu Glu
 355 360 365

Phe Asp Tyr Thr Pro Phe Gly Ile Glu Thr Thr Ala Asp Trp Gln Pro
 370 375 380

Phe Leu Pro Val Pro Glu Trp Ala Asp Glu Glu His Tyr Gln Leu Val
 385 390 395 400

Asp Leu Tyr Gly Glu Gly Ile Pro Gly Leu Leu Tyr Gln Asn Asn Asp
 405 410 415

His Trp His Tyr Arg Ser Pro Ala Arg Gly Asp Thr Pro Asp Gly Ile
 420 425 430

Ala Tyr Asn Ser Trp Arg Pro Leu Pro His Ile Pro Val Asn Ser Arg
 435 440 445

Asn Gly Met Leu Met Asp Leu Asn Gly Asp Gly Tyr Leu Glu Trp Leu
 450 455 460

Leu Ala Glu Pro Gly Val Ala Gly Arg Tyr Ser Met Asn Pro Asp Lys
 465 470 475 480

Ser Trp Ser Gly Phe Val Pro Leu Gln Ala Leu Pro Thr Glu Phe Phe
 485 490 495

His Pro Gln Ala Gln Leu Ala Asn Val Thr Gly Ser Gly Leu Thr Asp

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Leu Val Met Ile Gly Pro Lys Ser Val Arg Phe Tyr Ala Gly Glu Glu		
515	520	525
Ala Gly Phe Lys Arg Ala Cys Glu Val Trp Gln Gln Val Gly Ile Thr		
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Leu Pro Val Glu Arg Val Asp Lys Lys Glu Leu Val Ala Phe Ser Asp		
545	550	555
Met Leu Gly Ser Gly Gln Ser His Leu Val Arg Ile Arg His Asp Gly		
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Val Thr Cys Trp Pro Asn Leu Gly Asn Gly Val Phe Gly Ala Pro Leu		
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Ala Leu His Gly Phe Thr Ala Ser Glu Arg Glu Phe Asn Pro Glu Arg		
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Val Tyr Leu Val Asp Leu Asp Gly Ser Gly Ala Ser Asp Ile Ile Tyr		
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Ala Ser Arg Asp Ala Leu Leu Ile Tyr Arg Asn Leu Ser Gly Asn Gly		
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Phe Ala Asp Pro Val Arg Val Pro Leu Pro Asp Gly Val Arg Phe Asp		
	645	650
Asn Leu Cys Arg Leu Leu Pro Ala Asp Ile Arg Gly Leu Gly Val Ala		
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Ser Leu Val Leu His Val Pro Tyr Met Ala Pro Arg Ser Trp Lys Leu		
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Asp Phe Phe Ala Ala Lys Pro Tyr Leu Leu Gln Thr Val Ser Asn Asn		
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Leu Gly Ala Ser Ser Ser Phe Trp Tyr Arg Ser Ser Thr Gln Tyr Trp		
	705	710
Leu Asp Glu Lys Gln Ala Ala Ser Ser Ala Val Ser Ala Leu Pro Phe		
	725	730
		735

Pro Ile Asn Val Val Ser Asp Met His Thr Val Asp Glu Ile Ser Gly
 740 745 750

Arg Thr Arg Thr Gln Lys Tyr Thr Tyr Arg His Gly Val Tyr Asp Arg
 755 760 765

Thr Glu Lys Glu Phe Ala Gly Phe Gly Arg Ile Asp Thr Trp Glu Glu
 770 775 780

Glu Arg Asp Ser Glu Gly Thr Leu Ser Val Ser Thr Pro Pro Val Leu
 785 790 795 800

Thr Arg Thr Trp Tyr His Thr Gly Gln Lys Gln Asp Glu Glu Arg Ala
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Val Gln Gln Tyr Trp Gln Gly Asp Pro Ala Ala Phe Gln Val Lys Pro
 820 825 830

Val Arg Leu Thr Arg Phe Asp Ala Ala Ala Ala Gln Asp Leu Pro Leu
 835 840 845

Asp Ser Asn Asn Gly Gln Gln Glu Tyr Trp Leu Tyr Arg Ser Leu Gln
 850 855 860

Gly Met Pro Leu Arg Thr Glu Ile Phe Ala Gly Asp Val Gly Gly Ser
 865 870 875 880

Pro Pro Tyr Gln Val Glu Ser Phe Arg Tyr Gln Val Arg Leu Val Gln
 885 890 895

Ser Ile Asp Ser Glu Cys Val Ala Leu Pro Met Gln Leu Glu Gln Leu
 900 905 910

Thr Tyr Asn Tyr Glu Gln Ile Ala Ser Asp Pro Gln Cys Ser Gln Gln
 915 920 925

Ile Gln Gln Trp Phe Asp Glu Tyr Gly Val Ala Ala Gln Ser Val Thr
 930 935 940

Ile Gln Tyr Pro Arg Arg Ala Gln Pro Glu Asp Asn Pro Tyr Pro Arg
 945 950 955 960

Thr Leu Pro Asp Thr Ser Trp Ser Ser Ser Tyr Asp Ser Gln Gln Met
 965 970 975

Leu Leu Arg Leu Thr Arg Gln Arg Gln Lys Ala Tyr His Leu Ala Asp
 980 985 990

Pro Glu Gly Trp Arg Leu Asn Ile Pro His Gln Thr Arg Leu Asp Ala
 995 1000 1005

Phe Ile Tyr Ser Ala Asp Ser Val Pro Ala Glu Gly Ile Ser Ala
 1010 1015 1020

Glu Leu Leu Glu Val Asp Gly Thr Leu Arg Ser Ser Ala Leu Glu
 1025 1030 1035

Gln Ala Tyr Gly Gly Gln Ser Glu Ile Ile Tyr Ala Gly Gly Gly
 1040 1045 1050

Glu Pro Asp Leu Arg Ala Leu Val His Tyr Thr Arg Ser Ala Val
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Leu Asp Glu Asp Cys Leu Gln Ala Tyr Glu Gly Val Leu Ser Asp
 1070 1075 1080

Ser Gln Leu Asn Ser Leu Leu Ala Ser Ser Gly Tyr Gln Arg Ser
 1085 1090 1095

Ala Arg Ile Leu Gly Ser Gly Asp Glu Val Asp Ile Phe Val Ala
 1100 1105 1110

Glu Gln Gly Phe Thr Arg Tyr Ala Asp Glu Pro Asn Phe Phe Arg
 1115 1120 1125

Ile Leu Gly Gln Gln Ser Ser Leu Leu Ser Gly Glu Gln Val Leu
 1130 1135 1140

Thr Trp Asp Asp Asn Phe Cys Ala Val Thr Ser Ile Glu Asp Ala
 1145 1150 1155

Leu Gly Asn Gln Ile Gln Ile Ala Tyr Asp Tyr Arg Phe Val Glu
 1160 1165 1170

Ala Ile Gln Ile Thr Asp Thr Asn Asn Asn Val Asn Gln Val Ala
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Leu Asp Ala Leu Gly Arg Val Val Tyr Ser Arg Thr Trp Gly Thr
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1235						1240					1245			
Thr	Ile	Thr	Leu	Ala	Gln	Leu	Ser	Glu	Leu	Val	Pro	Asp	Ser	Glu
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Lys	Gln	Trp	Ser	Phe	Leu	Ile	Asp	Asn	Arg	Leu	Ile	Met	Pro	Asp
1265						1270					1275			
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Glu	Glu	Ala	Val	Ser	Ser	Ser	Met	Tyr	Ala	Thr	Ile	Tyr	Tyr	Tyr
1385						1390					1395			
Asp	Ala	Leu	Ala	Arg	Gln	Leu	Arg	Met	Val	Asn	Ala	Lys	Gly	Tyr
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1415

1420

1425

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<210> 12

<211> 2793

<212> DNA

<213> Paenibacillus strain IDAS 1529

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<210> 13

<211> 930

<212> PRT

<213> Paenibacillus strain IDAS 1529

<400> 13

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20          25          30

Ala Glu Asp Pro Ala Asp Glu Cys Ile Leu Arg Asn Thr Tyr Thr Pro
35          40          45

Leu Ser Tyr Leu Gly Ser Ser Met Asp Pro Arg Leu Phe Ser Gln Tyr
50          55          60

Gln Asp Asp Arg Gly Thr Pro Pro Asn Ile Arg Thr Met Ala Ser Leu
65          70          75          80

Arg Gly Glu Ala Leu Cys Ser Glu Ser Val Asp Ala Gly Arg Lys Ala
85          90          95

Glu Leu Phe Asp Ile Glu Gly Arg Pro Val Trp Leu Ile Asp Ala Asn
100         105         110

Gly Thr Glu Thr Thr Leu Glu Tyr Asp Val Leu Gly Arg Pro Thr Ala
115         120         125

Val Phe Glu Gln Gln Glu Gly Thr Asp Ser Pro Gln Cys Arg Glu Arg
130         135         140

Phe Ile Tyr Gly Glu Lys Glu Ala Asp Ala Gln Ala Asn Asn Leu Arg
145         150         155         160

Gly Gln Leu Val Arg His Tyr Asp Thr Ala Gly Arg Ile Gln Thr Asp
165         170         175

Ser Ile Ser Leu Ala Gly Leu Pro Leu Arg Gln Ser Arg Gln Leu Leu
180         185         190

Lys Asn Trp Asp Glu Pro Gly Asp Trp Ser Met Asp Glu Glu Ser Ala
195         200         205

Trp Ala Ser Leu Leu Ala Ala Glu Ala Tyr Asp Thr Ser Trp Arg Tyr
210         215         220

Asp Ala Gln Asp Arg Val Leu Ala Gln Thr Asp Ala Lys Gly Asn Leu
225         230         235         240

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Ile	Val	Lys	Arg	Ser	Thr	Arg	Lys	Thr	Gln	Thr	Thr	Thr	Gln	Thr	Asp
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Thr	Thr	Leu	Tyr	Leu	Pro	Gly	Leu	Glu	Leu	Arg	Ile	Arg	Gln	Thr	Gly
		515					520					525			
Asp	Arg	Val	Thr	Glu	Ala	Leu	Gln	Val	Ile	Thr	Val	Asp	Glu	Gly	Ala
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Gly	Gln	Val	Arg	Val	Leu	His	Trp	Glu	Asp	Gly	Thr	Glu	Pro	Gly	Gly
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Ile	Ala	Asn	Asp	Gln	Tyr	Arg	Tyr	Ser	Leu	Asn	Asp	His	Leu	Thr	Ser
				565					570					575	
Ser	Leu	Leu	Glu	Val	Asp	Gly	Gln	Gly	Gln	Ile	Ile	Ser	Lys	Glu	Glu
			580					585					590		
Phe	Tyr	Pro	Tyr	Gly	Gly	Thr	Ala	Leu	Trp	Thr	Ala	Arg	Ser	Glu	Val
		595					600					605			
Glu	Ala	Ser	Tyr	Lys	Thr	Ile	Arg	Tyr	Ser	Gly	Lys	Glu	Arg	Asp	Ala
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Thr	Gly	Leu	Tyr	Tyr	Tyr	Gly	His	Arg	Tyr	Tyr	Met	Pro	Trp	Leu	Gly
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Arg	Trp	Leu	Asn	Pro	Asp	Pro	Ala	Gly	Met	Val	Asp	Gly	Leu	Asn	Leu
				645					650					655	
Tyr	Arg	Met	Val	Arg	Asn	Asn	Pro	Ile	Gly	Leu	Met	Asp	Pro	Asn	Gly
			660					665					670		
Asn	Ala	Pro	Ile	Asn	Val	Ala	Asp	Tyr	Ser	Phe	Val	His	Gly	Asp	Leu
		675					680					685			
Val	Tyr	Gly	Leu	Ser	Lys	Glu	Arg	Gly	Arg	Tyr	Leu	Lys	Leu	Phe	Asn
	690					695					700				

Pro Asn Phe Asn Met Glu Lys Ser Asp Ser Pro Ala Met Val Ile Asp
 705 710 715 720

Gln Tyr Asn Asn Asn Val Ala Leu Ser Ile Thr Asn Gln Tyr Lys Val
 725 730 735

Glu Glu Leu Met Lys Phe Gln Lys Asp Pro Gln Lys Ala Ala Arg Lys
 740 745 750

Ile Lys Val Pro Glu Gly Asn Arg Leu Ser Arg Asn Glu Asn Tyr Pro
 755 760 765

Leu Trp His Asp Tyr Ile Asn Ile Gly Glu Ala Lys Ala Ala Phe Lys
 770 775 780

Ala Ser His Ile Phe Gln Glu Val Lys Gly Asn Tyr Gly Lys Asp Tyr
 785 790 795 800

Tyr His Lys Leu Leu Leu Asp Arg Met Ile Glu Ser Pro Leu Leu Trp
 805 810 815

Lys Arg Gly Ser Lys Leu Gly Leu Glu Ile Ala Ala Thr Asn Gln Arg
 820 825 830

Thr Lys Ile His Phe Val Leu Asp Asn Leu Asn Ile Glu Gln Val Val
 835 840 845

Thr Lys Glu Gly Ser Gly Gly Gln Ser Ile Thr Ala Ser Glu Leu Arg
 850 855 860

Tyr Ile Tyr Arg Asn Arg Glu Arg Leu Asn Gly Arg Val Ile Phe Tyr
 865 870 875 880

Arg Asn Asn Glu Arg Leu Asp Gln Ala Pro Trp Gln Glu Asn Pro Asp
 885 890 895

Leu Trp Ser Lys Tyr Gln Pro Gly Leu Arg Gln Ser Ser Ser Ser Arg
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Val Lys Glu Arg Gly Ile Gly Asn Phe Phe Arg Arg Phe Ser Met Lys
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Arg Lys
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 <211> 1791
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Nucleic acid sequence of ORF7, which encodes a cry-like protein.

<400> 14

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<210> 15

<211> 596

<212> PRT

<213> Artificial Sequence

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<223> Amino acid sequence encoded by ORF7.

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Val Gly Met Ser Leu Ile Ser Glu Leu Leu Gly Thr Val Pro Val Ala
35          40          45

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Gly Ser Ile Leu Gln Phe Val Phe Asp Lys Leu Trp Phe Ile Phe Gly
50          55          60

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Pro Ser Glu Trp Asp Ser Leu Met Glu His Val Glu Ala Leu Ile Asp
65          70          75          80

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Ser Lys Ile Gln Glu Gln Val Lys Arg Ser Ala Gln Asp Glu Leu Asn
85          90          95

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Ala Ile Thr Asn Asn Leu Ser Thr Tyr Leu Lys Phe Leu Asp Ala Trp
100         105         110

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```

Glu Asn Asp Ser Asn Asn Leu Arg Ala Arg Ala Val Val Lys Asp Gln
115         120         125

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Phe Val Gly Leu Glu Gln Thr Leu Glu Arg Lys Met Val Ser Val Phe
130         135         140

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Gly Ser Thr Gly His Glu Val His Leu Leu Pro Ile Phe Ala Gln Ala

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145		150		155		160									
Ala	Asn	Leu	His	Leu	Ile	Leu	Leu	Arg	Asp	Ala	Glu	Lys	Tyr	Gly	Lys
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Arg	Trp	Gly	Trp	Ala	Asp	Arg	Glu	Ile	Gln	Val	Tyr	Tyr	Asp	Asn	Gln
			180					185					190		
Ile	Arg	Tyr	Ile	His	Glu	Tyr	Thr	Asp	His	Cys	Ile	Lys	Tyr	Tyr	Asn
		195					200					205			
Gln	Gly	Leu	Ser	Lys	Leu	Lys	Gly	Ser	Thr	Tyr	Gln	Asp	Trp	Asp	Lys
	210					215					220				
Tyr	Asn	Arg	Phe	Arg	Arg	Glu	Met	Thr	Leu	Thr	Val	Leu	Asp	Leu	Ile
225					230					235					240
Ser	Ile	Phe	Pro	Ser	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Ile	Asp	Thr	Ile
				245					250					255	
Gly	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Ser	Asp	Leu	Leu	Ile	Ala	Asn	Pro
			260					265					270		
Ser	Gly	Met	Gln	Thr	Phe	Thr	Asn	Val	Asp	Phe	Asp	Asn	Ile	Leu	Ile
		275					280					285			
Arg	Lys	Pro	His	Leu	Met	Asp	Phe	Leu	Arg	Thr	Leu	Glu	Ile	Phe	Thr
	290					295					300				
Asp	Arg	His	Asn	Ala	Ser	Arg	His	Asn	Val	Tyr	Trp	Gly	Gly	His	Arg
305					310					315					320
Val	His	Ser	Ser	Tyr	Thr	Gly	Gly	Asn	Phe	Glu	Asn	Phe	Glu	Ser	Pro
				325					330					335	
Leu	Tyr	Gly	Ser	Glu	Ala	Asn	Val	Glu	Pro	Arg	Thr	Trp	Leu	Ser	Phe
			340					345					350		
Gly	Glu	Ser	Gln	Val	Tyr	Asn	Ile	Arg	Ser	Lys	Pro	Glu	Trp	Asp	Arg
		355					360					365			
Gly	Ser	Thr	Ala	Ile	Ser	Gly	Ser	Tyr	Glu	Phe	Arg	Gly	Val	Thr	Gly
	370					375					380				

Cys Ser Phe Tyr Arg Met Gly Asn Phe Ala Gly Thr Val Ala Leu Thr
 385 390 395 400

Tyr Arg Gln Phe Gly Asn Glu Gly Ser Gln Ile Pro Leu His Arg Leu
 405 410 415

Cys His Val Thr Tyr Phe Arg Arg Ser Gln Ala Val Gly Ala Thr Ser
 420 425 430

Arg Gln Thr Leu Thr Ser Gly Pro Leu Phe Ser Trp Thr His Ser Ser
 435 440 445

Ala Thr Glu Thr Asn Ile Ile His Pro Thr Lys Ile Thr Gln Ile Pro
 450 455 460

Met Val Lys Ala Ser Ser Leu Gly Ser Gly Thr Ser Val Val Gln Gly
 465 470 475 480

Pro Gly Phe Thr Gly Gly Asp Val Leu Arg Arg Asn Ser Pro Gly Ser
 485 490 495

Thr Gly Thr Leu Arg Val Asn Val Asn Ser Pro Leu Ser Gln Arg Tyr
 500 505 510

Arg Ile Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Asp Phe Phe Val
 515 520 525

Ile Arg Gly Asn Thr Thr Val Asn Asn Phe Arg Phe Gly Asn Thr Met
 530 535 540

Arg Lys Gly Asp Pro Ile Thr Ser Arg Ser Phe Arg Phe Ala Ala Phe
 545 550 555 560

Ser Thr Pro Phe Thr Phe Ala Ser Ser Gln Asp Glu Leu Arg Ile Asn
 565 570 575

Val Gln Asn Phe Asn Asn Gly Glu Glu Val Tyr Ile Asp Arg Ile Glu
 580 585 590

Val Ile Pro Val
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<210> 16
 <211> 1547
 <212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of the 16S rDNA of IDAS1529.

<400> 16

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gtaggttaacc tgcccttaag accgggataa ctacacgaaa cgtgggctaa taccggatag      180
gcgatttcct cgcattgagg aatcgggaaa ggcggaaccaa tctgccactt atggatggac      240
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cctgagaggg tgatcggcca cactgggact gagacacggc ccagactcct acgggaggca      360
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caaatcatca tgccccttat gacctgggct acacacgtac tacaatggct ggtacaacgg     1260
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atacgttccc ggggtcttgta cacaccgccc gtcacaccac gagagtttac aacacccgaa     1440
gtcgttgggg taaccgcaag gagccagccg ccgaagggtg ggtagatgat tggggtgaag     1500
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<210> 17
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> N-terminal amino acid sequence for the purified toxin from the
 broth fraction from IDAS1529.

<400> 17

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Arg Phe Gln Ala
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<210> 18
 <211> 379
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of thiaminase I from Bacillus
 thiaminolyticus.

<400> 18

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Pro Tyr Val Pro Asp Pro Ala Arg Phe Gln Ala Ala Val Leu Asp Gln
 20 25 30

Trp Gln Arg Gln Glu Pro Gly Val Lys Leu Glu Phe Thr Asp Trp Asp
 35 40 45

Ser Tyr Ser Ala Asp Pro Pro Asp Asp Leu Asp Val Phe Val Leu Asp
 50 55 60

Ser Ile Phe Leu Ser His Phe Val Asp Ala Gly Tyr Leu Leu Pro Phe
 65 70 75 80

Gly Ser Gln Asp Ile Asp Gln Ala Glu Asp Val Leu Pro Phe Ala Leu
 85 90 95

Gln Gly Ala Lys Arg Asn Gly Glu Val Tyr Gly Leu Pro Gln Ile Leu
 100 105 110

Cys Thr Asn Leu Leu Phe Tyr Arg Lys Gly Asp Leu Lys Ile Gly Gln

115							120									125
Val	Asp	Asn	Ile	Tyr	Glu	Leu	Tyr	Lys	Lys	Ile	Gly	Thr	Ser	His	Ser	
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Glu	Gln	Ile	Pro	Pro	Pro	Gln	Asn	Lys	Gly	Leu	Leu	Ile	Asn	Met	Ala	
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Gly	Gly	Thr	Thr	Lys	Ala	Ser	Met	Tyr	Leu	Glu	Ala	Leu	Ile	Asp	Val	
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Thr	Gly	Gln	Tyr	Thr	Glu	Tyr	Asp	Leu	Leu	Pro	Pro	Leu	Asp	Pro	Leu	
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Asn	Asp	Lys	Val	Ile	Arg	Gly	Leu	Arg	Leu	Leu	Ile	Asn	Met	Ala	Gly	
		195					200					205				
Glu	Lys	Pro	Ser	Gln	Tyr	Val	Pro	Glu	Asp	Gly	Asp	Ala	Tyr	Val	Arg	
	210					215					220					
Ala	Ser	Trp	Phe	Ala	Gln	Gly	Ser	Gly	Arg	Ala	Phe	Ile	Gly	Tyr	Ser	
225					230					235					240	
Glu	Ser	Met	Met	Arg	Met	Gly	Asp	Tyr	Ala	Glu	Gln	Val	Arg	Phe	Lys	
				245					250					255		
Pro	Ile	Ser	Ser	Ser	Ala	Gly	Gln	Asp	Ile	Pro	Leu	Phe	Tyr	Ser	Asp	
			260					265					270			
Val	Val	Ser	Val	Asn	Ser	Lys	Thr	Ala	His	Pro	Glu	Leu	Ala	Lys	Lys	
		275					280					285				
Leu	Ala	Asn	Val	Met	Ala	Ser	Ala	Asp	Thr	Val	Glu	Gln	Ala	Leu	Arg	
	290					295					300					
Pro	Gln	Ala	Asp	Gly	Gln	Tyr	Pro	Gln	Tyr	Leu	Leu	Pro	Ala	Arg	His	
305					310					315					320	
Gln	Val	Tyr	Glu	Ala	Leu	Met	Gln	Asp	Tyr	Pro	Ile	Tyr	Ser	Glu	Leu	
				325					330					335		
Ala	Gln	Ile	Val	Asn	Lys	Pro	Ser	Asn	Arg	Val	Phe	Arg	Leu	Gly	Pro	
			340					345					350			

Glu Val Arg Thr Trp Leu Lys Asp Ala Lys Gln Val Leu Pro Glu Ala
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Leu Gly Leu Thr Asp Val Ser Ser Leu Ala Ser
 370 375

<210> 19
 <211> 953
 <212> PRT
 <213> Paenibacillus strain IDAS 1529

<400> 19

Met Lys Met Ile Pro Trp Thr His His Tyr Leu Leu His Arg Leu Arg
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Gly Glu Met Glu Val Lys Pro Met Asn Thr Thr Ser Ile Tyr Arg Gly
 20 25 30

Thr Pro Thr Ile Ser Val Val Asp Asn Arg Asn Leu Glu Ile Arg Ile
 35 40 45

Leu Gln Tyr Asn Arg Ile Ala Ala Glu Asp Pro Ala Asp Glu Cys Ile
 50 55 60

Leu Arg Asn Thr Tyr Thr Pro Leu Ser Tyr Leu Gly Ser Ser Met Asp
 65 70 75 80

Pro Arg Leu Phe Ser Gln Tyr Gln Asp Asp Arg Gly Thr Pro Pro Asn
 85 90 95

Ile Arg Thr Met Ala Ser Leu Arg Gly Glu Ala Leu Cys Ser Glu Ser
 100 105 110

Val Asp Ala Gly Arg Lys Ala Glu Leu Phe Asp Ile Glu Gly Arg Pro
 115 120 125

Val Trp Leu Ile Asp Ala Asn Gly Thr Glu Thr Thr Leu Glu Tyr Asp
 130 135 140

Val Leu Gly Arg Pro Thr Ala Val Phe Glu Gln Gln Glu Gly Thr Asp
 145 150 155 160

Ser Pro Gln Cys Arg Glu Arg Phe Ile Tyr Gly Glu Lys Glu Ala Asp
 165 170 175

Ala Gln Ala Asn Asn Leu Arg Gly Gln Leu Val Arg His Tyr Asp Thr
 180 185 190

Ala Gly Arg Ile Gln Thr Asp Ser Ile Ser Leu Ala Gly Leu Pro Leu
 195 200 205

Arg Gln Ser Arg Gln Leu Leu Lys Asn Trp Asp Glu Pro Gly Asp Trp
 210 215 220

Ser Met Asp Glu Glu Ser Ala Trp Ala Ser Leu Leu Ala Ala Glu Ala
 225 230 235 240

Tyr Asp Thr Ser Trp Arg Tyr Asp Ala Gln Asp Arg Val Leu Ala Gln
 245 250 255

Thr Asp Ala Lys Gly Asn Leu Gln Gln Leu Thr Tyr Asn Asp Ala Gly
 260 265 270

Gln Pro Gln Ala Val Ser Leu Lys Leu Gln Gly Gln Ala Glu Gln Arg
 275 280 285

Ile Trp Asn Arg Ile Glu Tyr Asn Ala Ala Gly Gln Val Asp Leu Ala
 290 295 300

Glu Ala Gly Asn Gly Ile Val Thr Glu Tyr Thr Tyr Glu Glu Ser Thr
 305 310 315 320

Gln Arg Leu Ile Arg Lys Lys Asp Ser Arg Gly Leu Ser Ser Gly Glu
 325 330 335

Arg Glu Val Leu Gln Asp Tyr Arg Tyr Glu Tyr Asp Pro Val Gly Asn
 340 345 350

Ile Leu Ser Ile Tyr Asn Glu Ala Glu Pro Val Arg Tyr Phe Arg Asn
 355 360 365

Gln Ala Val Ala Pro Lys Arg Gln Tyr Ala Tyr Asp Ala Leu Tyr Gln
 370 375 380

Leu Val Ser Ser Ser Gly Arg Glu Ser Asp Ala Leu Arg Gln Gln Thr
 385 390 395 400

Ser Leu Pro Pro Leu Ile Thr Pro Ile Pro Leu Asp Asp Ser Gln Tyr
 405 410 415

Val Asn Tyr Ala Glu Lys Tyr Ser Tyr Asp Gln Ala Gly Asn Leu Ile
 420 425 430

Lys Leu Ser His Asn Gly Ala Ser Gln Tyr Thr Thr Asn Val Tyr Val
 435 440 445

Asp Lys Ser Ser Asn Arg Gly Ile Trp Arg Gln Gly Glu Asp Ile Pro
 450 455 460

Asp Ile Ala Ala Ser Phe Asp Arg Ala Gly Asn Gln Gln Ala Leu Phe
 465 470 475 480

Pro Gly Arg Pro Leu Glu Trp Asp Thr Arg Asn Gln Leu Ser Arg Val
 485 490 495

His Met Val Val Arg Glu Gly Gly Asp Asn Asp Trp Glu Gly Tyr Leu
 500 505 510

Tyr Asp Ser Ser Gly Met Arg Ile Val Lys Arg Ser Thr Arg Lys Thr
 515 520 525

Gln Thr Thr Thr Gln Thr Asp Thr Thr Leu Tyr Leu Pro Gly Leu Glu
 530 535 540

Leu Arg Ile Arg Gln Thr Gly Asp Arg Val Thr Glu Ala Leu Gln Val
 545 550 555 560

Ile Thr Val Asp Glu Gly Ala Gly Gln Val Arg Val Leu His Trp Glu
 565 570 575

Asp Gly Thr Glu Pro Gly Gly Ile Ala Asn Asp Gln Tyr Arg Tyr Ser
 580 585 590

Leu Asn Asp His Leu Thr Ser Ser Leu Leu Glu Val Asp Gly Gln Gly
 595 600 605

Gln Ile Ile Ser Lys Glu Glu Phe Tyr Pro Tyr Gly Gly Thr Ala Leu
 610 615 620

Trp Thr Ala Arg Ser Glu Val Glu Ala Ser Tyr Lys Thr Ile Arg Tyr
 625 630 635 640

Ser Gly Lys Glu Arg Asp Ala Thr Gly Leu Tyr Tyr Tyr Gly His Arg
 645 650 655

Tyr Tyr Met Pro Trp Leu Gly Arg Trp Leu Asn Pro Asp Pro Ala Gly
660 665 670

Met Val Asp Gly Leu Asn Leu Tyr Arg Met Val Arg Asn Asn Pro Ile
675 680 685

Gly Leu Met Asp Pro Asn Gly Asn Ala Pro Ile Asn Val Ala Asp Tyr
690 695 700

Ser Phe Val His Gly Asp Leu Val Tyr Gly Leu Ser Lys Glu Arg Gly
705 710 715 720

Arg Tyr Leu Lys Leu Phe Asn Pro Asn Phe Asn Met Glu Lys Ser Asp
725 730 735

Ser Pro Ala Met Val Ile Asp Gln Tyr Asn Asn Asn Val Ala Leu Ser
740 745 750

Ile Thr Asn Gln Tyr Lys Val Glu Glu Leu Met Lys Phe Gln Lys Asp
755 760 765

Pro Gln Lys Ala Ala Arg Lys Ile Lys Val Pro Glu Gly Asn Arg Leu
770 775 780

Ser Arg Asn Glu Asn Tyr Pro Leu Trp His Asp Tyr Ile Asn Ile Gly
785 790 795 800

Glu Ala Lys Ala Ala Phe Lys Ala Ser His Ile Phe Gln Glu Val Lys
805 810 815

Gly Asn Tyr Gly Lys Asp Tyr Tyr His Lys Leu Leu Leu Asp Arg Met
820 825 830

Ile Glu Ser Pro Leu Leu Trp Lys Arg Gly Ser Lys Leu Gly Leu Glu
835 840 845

Ile Ala Ala Thr Asn Gln Arg Thr Lys Ile His Phe Val Leu Asp Asn
850 855 860

Leu Asn Ile Glu Gln Val Val Thr Lys Glu Gly Ser Gly Gly Gln Ser
865 870 875 880

Ile Thr Ala Ser Glu Leu Arg Tyr Ile Tyr Arg Asn Arg Glu Arg Leu

885

890

895

Asn Gly Arg Val Ile Phe Tyr Arg Asn Asn Glu Arg Leu Asp Gln Ala
 900 905 910

Pro Trp Gln Glu Asn Pro Asp Leu Trp Ser Lys Tyr Gln Pro Gly Leu
 915 920 925

Arg Gln Ser Ser Ser Ser Arg Val Lys Glu Arg Gly Ile Gly Asn Phe
 930 935 940

Phe Arg Arg Phe Ser Met Lys Arg Lys
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<210> 20

<211> 4482

<212> DNA

<213> Xenorhabdus strain Xwi

<400> 20

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<210> 21

<211> 3051

<212> DNA

<213> Xenorhabdus strain Xwi

<400> 21

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atattgggtc atagggaaaa tacgacgcct gatcaggaat tctaccgtta tgatgcagac     1500
agtcagcgtg tcattaagac tcatattcag aagacaggta acagtgagca aatacagcga     1560
acattatatt tgccagagct ggaatggcgc acgacatata gcggcaatac attaaaagag     1620

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<210> 22
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<212> DNA
<213> Artificial Sequence

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<220>
<223> Primer SB101

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<400> 22
gckatggcsg acccgatgca wtacaagctg gc

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32

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<220>
 <223> Primer SB102

<400> 23
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32

<210> 24
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer SB103

<400> 24
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28

<210> 25
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer SB104

<400> 25
 tcraaaggca graamcggct gtcggt

26

<210> 26
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer SB105

<400> 26
 cttcyctkga tatcykytg gatgtgct

28

<210> 27
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 <212> DNA
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<220>
 <223> Primer SB106

<400> 27

acgrctgggya ttggyaatca gccartccaa

30

<210> 28
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer SB212

<220>
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 <222> (7)..(7)
 <223> n = i (inosine)

<400> 28
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27

<210> 29
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer SB213

<220>
 <221> misc_feature
 <222> (17)..(17)
 <223> n = i (inosine)

<400> 29
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25

<210> 30
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer SB215

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> n = i (inosine)

<400> 30
 cghagctcyn cccagtwytg gctggatgar aaa

33

<210> 31
 <211> 32

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer SB217

<220>
 <221> misc_feature
 <222> (24)..(24)
 <223> n = i (inosine)

<400> 31
 gtrtcatttt catcttcrtt bacnryaaac ca 32

<210> 32
 <211> 1293
 <212> DNA
 <213> Paenibacillus apairus strain DB482

<400> 32
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 tccctatgat gacgaccttg cgcaaataca tgccgtggcg gaggcgcact catctaattt 120
 gctgggggatt tgggataccc tgctggacac gcagcggact tccatcctgc agaattccgc 180
 cgctgcctgc cggataagca aggcgcggca atcggcatcc ccggatcaga gaggcctccga 240
 tgatgagccg gtattgatta caggagaaga attctacctg gagacgggcg gcaaaccggct 300
 ttttctggcg cataaactcg agataggctc cacgataagc gccaaaatca acattggacc 360
 gccgcaagcg gccgatatcg cgccagcaaa gttgcaactc gtttattacg gcagaggcgg 420
 cagagggggac tacttccttc gtgtggcaga cgatgtgtcc ctccgtggaa aattgctgaa 480
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 aatgattaat cgaggcaccg gcagcatgcc cagcgggact cacctgccag ttcagattga 600
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 gttgaccttt accctaagaa agaatgagtc cggacaagat accatttcca taatcgatat 780
 gatgccgcct gttgccgaca cgaccccgct cccgccgacg agggaaacgc tttccttgac 840
 gccaaacagc ttccgtctgc tgggtaaccc cgagccgaca gaagaagaca tcgccaagca 900
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 tgtcgatgat ttctgcatga agaccggctt gagctttgat gaattgctga acttaacgat 1020
 gcagaaggat tatcagtcaa aaagcagtga gtacaaaagc cgatttgtaa aatttggcgg 1080
 cggggagcat gttccggttt caacctatgg agctgtgttt ttgacaggta cggaagaaac 1140

tccgttgtgg gcaaaacagt ataacagcgc aggcgctgca acagacaccc ctgttttgaa 1200
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<210> 33
 <211> 430
 <212> PRT
 <213> Paenibacillus apairius strain DB482

<400> 33

Gln Pro Glu Gly Ser Gly Thr Leu Ala Ser Leu Lys Asp Thr Tyr His
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Pro Met Thr Leu Pro Tyr Asp Asp Asp Leu Ala Gln Ile Asn Ala Val
 20 25 30

Ala Glu Ala His Ser Ser Asn Leu Leu Gly Ile Trp Asp Thr Leu Leu
 35 40 45

Asp Thr Gln Arg Thr Ser Ile Leu Gln Asn Ser Ala Ala Ala Cys Arg
 50 55 60

Ile Ser Lys Ala Arg Gln Ser Ala Ser Pro Asp Gln Arg Ala Ser Asp
 65 70 75 80

Asp Glu Pro Val Leu Ile Thr Gly Glu Glu Phe Tyr Leu Glu Thr Gly
 85 90 95

Gly Lys Arg Leu Phe Leu Ala His Lys Leu Glu Ile Gly Ser Thr Ile
 100 105 110

Ser Ala Lys Ile Asn Ile Gly Pro Pro Gln Ala Ala Asp Ile Ala Pro
 115 120 125

Ala Lys Leu Gln Leu Val Tyr Tyr Gly Arg Gly Gly Arg Gly Asp Tyr
 130 135 140

Phe Leu Arg Val Ala Asp Asp Val Ser Leu Gly Gly Lys Leu Leu Asn
 145 150 155 160

Asn Cys Tyr Leu Thr Ser Asp Asp Gly Gln Ser Asn Asn Ile Asn Gly
 165 170 175

Pro Phe Cys Leu Met Ile Asn Arg Gly Thr Gly Ser Met Pro Ser Gly
 180 185 190

Thr His Leu Pro Val Gln Ile Asp Arg Val Thr Asp Thr Ser Leu Arg
 195 200 205

Ile Phe Val Pro Gln His Gly Tyr Leu Gly Leu Gly Glu Ser Leu Ala
 210 215 220

Ser Asn Trp Asn Glu Pro Leu Ala Leu Asn Leu Asp Leu Asp Gln Ala
 225 230 235 240

Leu Thr Phe Thr Leu Arg Lys Asn Glu Ser Gly Gln Asp Thr Ile Ser
 245 250 255

Ile Ile Asp Met Met Pro Pro Val Ala Asp Thr Thr Pro Ser Pro Pro
 260 265 270

Thr Arg Glu Thr Leu Ser Leu Thr Pro Asn Ser Phe Arg Leu Leu Val
 275 280 285

Asn Pro Glu Pro Thr Glu Glu Asp Ile Ala Lys His Tyr Asn Val Lys
 290 295 300

Thr Ala Ile Thr Arg Ala Pro Ala Asp Leu Ala Ala Ala Leu Asn Val
 305 310 315 320

Val Asp Asp Phe Cys Met Lys Thr Gly Leu Ser Phe Asp Glu Leu Leu
 325 330 335

Asn Leu Thr Met Gln Lys Asp Tyr Gln Ser Lys Ser Ser Glu Tyr Lys
 340 345 350

Ser Arg Phe Val Lys Phe Gly Gly Gly Glu His Val Pro Val Ser Thr
 355 360 365

Tyr Gly Ala Val Phe Leu Thr Gly Thr Glu Glu Thr Pro Leu Trp Ala
 370 375 380

Lys Gln Tyr Asn Ser Ala Gly Ala Ala Thr Asp Thr Pro Val Leu Asn
 385 390 395 400

Phe Thr Ala Asp Asn Val Ala Ala Leu Ala Gly Arg Ala Glu Lys Leu
 405 410 415

Val Arg Leu Ala Arg Ser Thr Gly Leu Ser Phe Glu Gln Leu
 420 425 430

<210> 34
 <211> 340
 <212> DNA
 <213> Paenibacillus apairius strain DB482

<400> 34
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 ggagcgggat actctgaccg aagccaagat gtattacatc caggccagcc aactgcttgg 120
 tccccgcccc gatatccgga tcaatcacag ttggcctaatt ccgaccctgc aaagcgaagc 180
 ggacgcggtg accgccgtac cgacgcgaag cgattcgcgg gcaacgcaa tctctgcctt 240
 gcgagcgctt ctgaaagcgg aaaacgggca tttcctgcgg ctttataatg atgaactgtt 300
 agctttcttg gataaaatcg atctgcgttt atacaattta 340

<210> 35
 <211> 565
 <212> DNA
 <213> Paenibacillus apairius strain DB482

<400> 35
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 tttagagaaa gaaatcggca ctgataaaac ggggtggagtt ttcaccctcc cggcctggaa 120
 tgatctgtat cagggattac tggcggggga ggcgctgctg ctcgagcttc agaagctgga 180
 gaatctgtgg ctggaggaag acaagcgcgg aatggaagcc gtaaaaacgg tatctttaga 240
 tacccttctc cgcaaagaaa cgccagagtc tagcttcgta gagctagtca aggaagttct 300
 ggacggaaag acgcctgacc ctgtaggcgg agtcggcgta cagctgcaaa acaatatttt 360
 cagcgcaacc cttgacctgt ccgttcttgg cttggatcgc tcttacaacc aagcggaaaa 420
 gacccgcagg atcaaaaatc tgtcgggttac cttaccgcg cttttgggac cttaccagga 480
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 cagcggttg ttcatacagg atctt 565

<210> 36
 <211> 113
 <212> PRT
 <213> Paenibacillus apairius strain DB482

<400> 36

Ile Phe Ile His Thr Leu Asp Phe Leu Ile Asn Arg Gly Asp Ser Leu

1 5 10 15
 Tyr Arg Leu Leu Glu Arg Asp Thr Leu Thr Glu Ala Lys Met Tyr Tyr
 20 25 30
 Ile Gln Ala Ser Gln Leu Leu Gly Pro Arg Pro Asp Ile Arg Ile Asn
 35 40 45
 His Ser Trp Pro Asn Pro Thr Leu Gln Ser Glu Ala Asp Ala Val Thr
 50 55 60
 Ala Val Pro Thr Arg Ser Asp Ser Arg Ala Thr Pro Ile Leu Ala Leu
 65 70 75 80
 Arg Ala Leu Leu Lys Ala Glu Asn Gly His Phe Leu Pro Pro Tyr Asn
 85 90 95
 Asp Glu Leu Leu Ala Phe Trp Asp Lys Ile Asp Leu Arg Leu Tyr Asn
 100 105 110

Leu

<210> 37
 <211> 188
 <212> PRT
 <213> Paenibacillus apairius strain DB482

<400> 37

Ser Leu Tyr Tyr Gln Met Tyr Asp Ala Ala Leu Pro Leu Cys Leu Met
 1 5 10 15
 Ala Lys Gln Ala Leu Glu Lys Glu Ile Gly Thr Asp Lys Thr Gly Gly
 20 25 30
 Val Phe Thr Leu Pro Ala Trp Asn Asp Leu Tyr Gln Gly Leu Leu Ala
 35 40 45
 Gly Glu Ala Leu Leu Leu Glu Leu Gln Lys Leu Glu Asn Leu Trp Leu
 50 55 60
 Glu Glu Asp Lys Arg Gly Met Glu Ala Val Lys Thr Val Ser Leu Asp
 65 70 75 80
 Thr Leu Leu Arg Lys Glu Thr Pro Glu Ser Ser Phe Val Glu Leu Val

85

90

95

Lys Glu Val Leu Asp Gly Lys Thr Pro Asp Pro Val Gly Gly Val Gly
 100 105 110

Val Gln Leu Gln Asn Asn Ile Phe Ser Ala Thr Leu Asp Leu Ser Val
 115 120 125

Leu Gly Leu Asp Arg Ser Tyr Asn Gln Ala Glu Lys Thr Arg Arg Ile
 130 135 140

Lys Asn Leu Ser Val Thr Leu Pro Ala Leu Leu Gly Pro Tyr Gln Asp
 145 150 155 160

Ile Glu Ala Thr Leu Ser Leu Gly Gly Glu Thr Val Ala Leu Ser His
 165 170 175

Gly Val Asp Asp Ser Gly Leu Phe Ile Thr Asp Leu
 180 185

<210> 38

<211> 2091

<212> DNA

<213> Paenibacillus apairius strain DB482

<400> 38

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 gtgtatgacc ggaccgataa ggaatttgcc ggggttcggcc acattgacac atgggaagag 180
 gagcgggatt ccgaggggaac ccttagcatc agcactcccc ccgtgctgac acggacctgg 240
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 cctgccgctt ttcagggttaa acccgtccgg cttactcgat tcgatgcggc aacggcccag 360
 gatgtccgc tagactctcc caataggcgg gaagagtatt ggctgtatcg ctcgttgcca 420
 gggatgccgc tgcgtaatga aatttttgct ggagatgttg tggggttgcc tccttatcag 480
 gtggagagct tacgttatca agtgcgcttg atgcagagca ccgattcgga atgtgttaca 540
 ttgcccattgc agttggagca gcttacgtac aactatgagc aaatcgccctc tgatccgcag 600
 tgttcacagc agatacagca atggttcgac gaatacggcg tggcggcaca gagtataacg 660
 atccaatatc cgcgcggggc acagccggag gacaatccgt accctcacac gctgccggat 720
 accagctgga gcagcagtta tgattcgag caaatgctgc tgcgggtaac aaggcaaagg 780

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caaaaagcgt accaccttgc agaccctgaa ggctggcgct tgaatatccc ccatcagaca      840
cgcttgatt ctttcatcta ttctgctgac agcgtgcctg ccgaaggaat aagcgcagag      900
ctgctggggg gtgacggcac gttacgatct ccggcgctgg aacaggctta tggcggccag      960
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agaagcgga ttctcgatga agcctgtttg caagcctatg aaggcgctact gagcgatagc     1080
caattgaact cgcttcttgc atcttccggc tatcaacgaa gcgcaagaat attgggttcc     1140
ggcgatgaag cggatatttt tgttgcgga caaggattta cccgttatgc ggatgaacag     1200
aattttttcc gtattctggg acaacaatcc tctctcttga ccggggaaca agtattaaca     1260
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gaggcggacc gtaagccgcc gcatacggtg gttttggcag cagatcgcta cccggatgac     1800
ccatcccagc aaattcaggc cagcgtcgtg tttagcgatg gctttgggcg tacgatacaa     1860
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ggagccgtaa tccgaagctt tcagcctttt tatattgatg actggaatta tgtgggcaaa     1980
gaggctgtca gcggctctat gtatgcaacg atctattact atgatgctct ggcacgccaa     2040
ctaaggatgg tcaacgcaa aggatatgag aggagaactg ctttttacc a                2091

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<210> 39
<211> 697
<212> PRT
<213> Paenibacillus apairius strain DB482

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<400> 39
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Gln Ala Thr Ser Ser Ala Val Cys Gly Val Pro Phe Pro Ile Asn Val
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Val Ser Asp Ile His Thr Val Asp Glu Ile Ser Gly Ser Ala Arg Ile
20          25          30

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Gln Lys Tyr Thr Tyr Arg Asn Gly Val Tyr Asp Arg Thr Asp Lys Glu
 35 40 45

Phe Ala Gly Phe Gly His Ile Asp Thr Trp Glu Glu Glu Arg Asp Ser
 50 55 60

Glu Gly Thr Leu Ser Ile Ser Thr Pro Pro Val Leu Thr Arg Thr Trp
 65 70 75 80

Tyr His Thr Gly Gln Lys Gln Asp Glu Glu Arg Ala Val Gln Gln Tyr
 85 90 95

Trp Gln Gly Asp Pro Ala Ala Phe Gln Val Lys Pro Val Arg Leu Thr
 100 105 110

Arg Phe Asp Ala Ala Thr Ala Gln Asp Val Pro Leu Asp Ser Pro Asn
 115 120 125

Arg Arg Glu Glu Tyr Trp Leu Tyr Arg Ser Leu Arg Gly Met Pro Leu
 130 135 140

Arg Asn Glu Ile Phe Ala Gly Asp Val Val Gly Leu Pro Pro Tyr Gln
 145 150 155 160

Val Glu Ser Leu Arg Tyr Gln Val Arg Leu Met Gln Ser Thr Asp Ser
 165 170 175

Glu Cys Val Thr Leu Pro Met Gln Leu Glu Gln Leu Thr Tyr Asn Tyr
 180 185 190

Glu Gln Ile Ala Ser Asp Pro Gln Cys Ser Gln Gln Ile Gln Gln Trp
 195 200 205

Phe Asp Glu Tyr Gly Val Ala Ala Gln Ser Ile Thr Ile Gln Tyr Pro
 210 215 220

Arg Arg Ala Gln Pro Glu Asp Asn Pro Tyr Pro His Thr Leu Pro Asp
 225 230 235 240

Thr Ser Trp Ser Ser Ser Tyr Asp Ser Gln Gln Met Leu Leu Arg Leu
 245 250 255

Thr Arg Gln Arg Gln Lys Ala Tyr His Leu Ala Asp Pro Glu Gly Trp
 260 265 270

Arg Leu Asn Ile Pro His Gln Thr Arg Leu Asp Ser Phe Ile Tyr Ser
 275 280 285

Ala Asp Ser Val Pro Ala Glu Gly Ile Ser Ala Glu Leu Leu Gly Gly
 290 295 300

Asp Gly Thr Leu Arg Ser Pro Ala Leu Glu Gln Ala Tyr Gly Gly Gln
 305 310 315 320

Ser Glu Ile Ile Tyr Ala Gly Gly Gly Glu Pro Asp Ser Arg Ala Leu
 325 330 335

Val His Tyr Thr Arg Ser Ala Ile Leu Asp Glu Ala Cys Leu Gln Ala
 340 345 350

Tyr Glu Gly Val Leu Ser Asp Ser Gln Leu Asn Ser Leu Leu Ala Ser
 355 360 365

Ser Gly Tyr Gln Arg Ser Ala Arg Ile Leu Gly Ser Gly Asp Glu Ala
 370 375 380

Asp Ile Phe Val Ala Glu Gln Gly Phe Thr Arg Tyr Ala Asp Glu Gln
 385 390 395 400

Asn Phe Phe Arg Ile Leu Gly Gln Gln Ser Ser Leu Leu Thr Gly Glu
 405 410 415

Gln Val Leu Thr Trp Asp Asp Asn Phe Cys Ala Val Thr Ser Ile Glu
 420 425 430

Asp Ala Leu Gly Asn Gln Ile Gln Ile Ala Tyr Asp Tyr Arg Phe Val
 435 440 445

Glu Ala Ile Gln Ile Thr Asp Ala Asn Asn Asn Val Asn Gln Val Ser
 450 455 460

Leu Asp Ala Leu Gly Arg Val Val Tyr Ser Arg Thr Trp Gly Thr Glu
 465 470 475 480

Glu Gly Ile Glu Thr Gly Phe Arg Pro Glu Ala Glu Phe Ser Pro Pro
 485 490 495

Glu Thr Met Glu Gln Ala Leu Ala Leu Ala Ser Pro Leu Pro Val Ala

500 505 510
 Ser Cys Cys Val Tyr Asp Ala His Ser Trp Met Gly Thr Ile Thr Leu
 515 520 525

 Gly Gln Leu Ser Ala Leu Val Pro Asp Ser Glu Lys Gln Trp Ser Phe
 530 535 540

 Leu Ile Ala Asn Arg Leu Ile Met Pro Asp Gly Arg Ile Arg Ala Arg
 545 550 555 560

 Gly Arg Ala Pro Trp Trp Leu Gln Arg Leu Leu Pro Pro Ala Val Ala
 565 570 575

 Lys Leu Leu Ser Glu Ala Asp Arg Lys Pro Pro His Thr Val Val Leu
 580 585 590

 Ala Ala Asp Arg Tyr Pro Asp Asp Pro Ser Gln Gln Ile Gln Ala Ser
 595 600 605

 Val Val Phe Ser Asp Gly Phe Gly Arg Thr Ile Gln Thr Ala Lys Arg
 610 615 620

 Ala Asp Thr Arg Trp Ala Ile Thr Glu Arg Ile Asp Tyr Asp Glu Thr
 625 630 635 640

 Gly Ala Val Ile Arg Ser Phe Gln Pro Phe Tyr Ile Asp Asp Trp Asn
 645 650 655

 Tyr Val Gly Lys Glu Ala Val Ser Gly Ser Met Tyr Ala Thr Ile Tyr
 660 665 670

 Tyr Tyr Asp Ala Leu Ala Arg Gln Leu Arg Met Val Asn Ala Lys Gly
 675 680 685

 Tyr Glu Arg Arg Thr Ala Phe Tyr Pro
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<210> 40
 <211> 858
 <212> DNA
 <213> Paenibacillus apairius strain DB482

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<213> Paenibacillus apairius strain DB482

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<212> DNA

<213> Photorhabdus strain W14

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<210> 43

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<212> DNA

<213> Photorhabdus strain W14

<400> 43

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 <211> 2748
 <212> DNA
 <213> Photorhabdus strain W14

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<210> 46
<211> 2883
<212> DNA
<213> Photorhabdus strain W14

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<211> 2850

<212> DNA

<213> Photorhabdus strain W14

<400> 47

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<212> DNA

<213> Photorhabdus strain W14

<400> 48

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 20 25 30

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 35 40 45

Leu Tyr His Glu Thr Ile Glu Gln Lys Lys Asn Asn Arg Leu Leu Glu
 50 55 60

Ala Arg Ile Phe Thr Arg Ala Asn Pro Gln Leu Ser Gly Ala Ile Arg
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Leu Gly Ile Glu Arg Asp Ser Val Ser Arg Ser Tyr Asp Glu Met Phe
 85 90 95

Gly Ala Arg Ser Ser Ser Phe Val Lys Pro Gly Ser Val Ala Ser Met
 100 105 110

Phe Ser Pro Ala Gly Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Lys Asp
 115 120 125

Leu His Phe Ser Ser Ser Ala Tyr His Leu Asp Asn Arg Arg Pro Asp
 130 135 140

Leu Ala Asp Leu Thr Leu Ser Gln Ser Asn Met Asp Thr Glu Ile Ser
 145 150 155 160

Thr Leu Thr Leu Ser Asn Glu Leu Leu Leu Glu His Ile Thr Arg Lys
 165 170 175

Thr Gly Gly Asp Ser Asp Ala Leu Met Glu Ser Leu Ser Thr Tyr Arg
 180 185 190

Gln Ala Ile Asp Thr Pro Tyr His Gln Pro Tyr Glu Thr Ile Arg Gln
 195 200 205

Val Ile Met Thr His Asp Ser Thr Leu Ser Ala Leu Ser Arg Asn Pro
 210 215 220

Glu Val Met Gly Gln Ala Glu Gly Ala Ser Leu Leu Ala Ile Leu Ala

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225                230                235                240

Asn Ile Ser Pro Glu Leu Tyr Asn Ile Leu Thr Glu Glu Ile Thr Glu
                245                250                255

Lys Asn Ala Asp Ala Leu Phe Ala Gln Asn Phe Ser Glu Asn Ile Thr
                260                265                270

Pro Glu Asn Phe Ala Ser Gln Ser Trp Ile Ala Lys Tyr Tyr Gly Leu
                275                280                285

Glu Leu Ser Glu Val Gln Lys Tyr Leu Gly Met Leu Gln Asn Gly Tyr
                290                295                300

Ser Asp Ser Thr Ser Ala Tyr Val Asp Asn Ile Ser Thr Gly Leu Val
305                310                315                320

Val Asn Asn Glu Ser Lys Leu Glu Ala Tyr Lys Ile Thr Arg Val Lys
                325                330                335

Thr Asp Asp Tyr Asp Lys Asn Ile Asn Tyr Phe Asp Leu Met Tyr Glu
                340                345                350

Gly Asn Asn Gln Phe Phe Ile Arg Ala Asn Phe Lys Val Ser Arg Glu
                355                360                365

Phe Gly Ala Thr Leu Arg Lys Asn Ala Gly Pro Ser Gly Ile Val Gly
                370                375                380

Ser Leu Ser Gly Pro Leu Ile Ala Asn Thr Asn Phe Lys Ser Asn Tyr
385                390                395                400

Leu Ser Asn Ile Ser Asp Ser Glu Tyr Lys Asn Gly Val Lys Ile Tyr
                405                410                415

Ala Tyr Arg Tyr Thr Ser Ser Thr Ser Ala Thr Asn Gln Gly Gly Gly
                420                425                430

Ile Phe Thr Phe Glu Ser Tyr Pro Leu Thr Ile Phe Ala Leu Lys Leu
                435                440                445

Asn Lys Ala Ile Arg Leu Cys Leu Thr Ser Gly Leu Ser Pro Asn Glu
                450                455                460

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Leu Gln Thr Ile Val Arg Ser Asp Asn Ala Gln Gly Ile Ile Asn Asp
465 470 475 480

Ser Val Leu Thr Lys Val Phe Tyr Thr Leu Phe Tyr Ser His Arg Tyr
485 490 495

Ala Leu Ser Phe Asp Asp Ala Gln Val Leu Asn Gly Ser Val Ile Asn
500 505 510

Gln Tyr Ala Asp Asp Asp Ser Val Ser His Phe Asn Arg Leu Phe Asn
515 520 525

Thr Pro Pro Leu Lys Gly Lys Ile Phe Glu Ala Asp Gly Asn Thr Val
530 535 540

Ser Ile Asp Pro Asp Glu Glu Gln Ser Thr Phe Ala Arg Ser Ala Leu
545 550 555 560

Met Arg Gly Leu Gly Val Asn Ser Gly Glu Leu Tyr Gln Leu Gly Lys
565 570 575

Leu Ala Gly Val Leu Asp Ala Gln Asn Thr Ile Thr Leu Ser Val Phe
580 585 590

Val Ile Ser Ser Leu Tyr Arg Leu Thr Leu Leu Ala Arg Val His Gln
595 600 605

Leu Thr Val Asn Glu Leu Cys Met Leu Tyr Gly Leu Ser Pro Phe Asn
610 615 620

Gly Lys Thr Thr Ala Ser Leu Ser Ser Gly Glu Leu Pro Arg Leu Val
625 630 635 640

Ile Trp Leu Tyr Gln Val Thr Gln Trp Leu Thr Glu Ala Glu Ile Thr
645 650 655

Thr Glu Ala Ile Trp Leu Leu Cys Thr Pro Glu Phe Ser Gly Asn Ile
660 665 670

Ser Pro Glu Ile Ser Asn Leu Leu Asn Asn Leu Arg Pro Ser Ile Ser
675 680 685

Glu Asp Met Ala Gln Ser His Asn Arg Glu Leu Gln Ala Glu Ile Leu
690 695 700

Ala Pro Phe Ile Ala Ala Thr Leu His Leu Ala Ser Pro Asp Met Ala
 705 710 715 720
 Arg Tyr Ile Leu Leu Trp Thr Asp Asn Leu Arg Pro Gly Gly Leu Asp
 725 730 735
 Ile Ala Gly Phe Met Thr Leu Val Leu Lys Glu Ser Leu Asn Ala Asn
 740 745 750
 Glu Thr Thr Gln Leu Val Gln Phe Cys His Val Met Ala Gln Leu Ser
 755 760 765
 Leu Ser Val Gln Thr Leu Arg Leu Ser Glu Ala Glu Leu Ser Val Leu
 770 775 780
 Val Ile Ser Gly Phe Ala Val Leu Gly Ala Lys Asn Gln Pro Ala Gly
 785 790 795 800
 Gln His Asn Ile Asp Thr Leu Phe Ser Leu Tyr Arg Phe His Gln Trp
 805 810 815
 Ile Asn Gly Leu Gly Asn Pro Gly Ser Asp Thr Leu Asp Met Leu Arg
 820 825 830
 Gln Gln Thr Leu Thr Ala Asp Arg Leu Ala Ser Val Met Gly Leu Asp
 835 840 845
 Ile Ser Met Val Thr Gln Ala Met Val Ser Ala Gly Val Asn Gln Leu
 850 855 860
 Gln Cys Trp Gln Asp Ile Asn Thr Val Leu Gln Trp Ile Asp Val Ala
 865 870 875 880
 Ser Ala Leu His Thr Met Pro Ser Val Ile Arg Thr Leu Val Asn Ile
 885 890 895
 Arg Tyr Val Thr Ala Leu Asn Lys Ala Glu Ser Asn Leu Pro Ser Trp
 900 905 910
 Asp Glu Trp Gln Thr Leu Ala Glu Asn Met Glu Ala Gly Leu Ser Thr
 915 920 925
 Gln Gln Ala Gln Thr Leu Ala Asp Tyr Thr Ala Glu Arg Leu Ser Ser
 930 935 940

Val Leu Cys Asn Trp Phe Leu Ala Asn Ile Gln Pro Glu Gly Val Ser
 945 950 955 960

Leu His Ser Arg Asp Asp Leu Tyr Ser Tyr Phe Leu Ile Asp Asn Gln
 965 970 975

Val Ser Ser Ala Ile Lys Thr Thr Arg Leu Ala Glu Ala Ile Ala Gly
 980 985 990

Ile Gln Leu Tyr Ile Asn Arg Ala Leu Asn Arg Ile Glu Pro Asn Ala
 995 1000 1005

Arg Ala Asp Val Ser Thr Arg Gln Phe Phe Thr Asp Trp Thr Val
 1010 1015 1020

Asn Asn Arg Tyr Ser Thr Trp Gly Gly Val Ser Arg Leu Val Tyr
 1025 1030 1035

Tyr Pro Glu Asn Tyr Ile Asp Pro Thr Gln Arg Ile Gly Gln Thr
 1040 1045 1050

Arg Met Met Asp Glu Leu Leu Glu Asn Ile Ser Gln Ser Lys Leu
 1055 1060 1065

Ser Arg Asp Thr Val Glu Asp Ala Phe Lys Thr Tyr Leu Thr Arg
 1070 1075 1080

Phe Glu Thr Val Ala Asp Leu Lys Val Val Ser Ala Tyr His Asp
 1085 1090 1095

Asn Val Asn Ser Asn Thr Gly Leu Thr Trp Phe Val Gly Gln Thr
 1100 1105 1110

Arg Glu Asn Leu Pro Glu Tyr Tyr Trp Arg Asn Val Asp Ile Ser
 1115 1120 1125

Arg Met Gln Ala Gly Glu Leu Ala Ala Asn Ala Trp Lys Glu Trp
 1130 1135 1140

Thr Lys Ile Asp Thr Ala Val Asn Pro Tyr Lys Asp Ala Ile Arg
 1145 1150 1155

Pro Val Ile Phe Arg Glu Arg Leu His Leu Ile Trp Val Glu Lys

1160		1165		1170
Glu Glu Val Ala Lys Asn Gly Thr Asp Pro Val Glu Thr Tyr Asp				
1175		1180		1185
Arg Phe Thr Leu Lys Leu Ala Phe Leu Arg His Asp Gly Ser Trp				
1190		1195		1200
Ser Ala Pro Trp Ser Tyr Asp Ile Thr Thr Gln Val Glu Ala Val				
1205		1210		1215
Thr Asp Lys Lys Pro Asp Thr Glu Arg Leu Ala Leu Ala Ala Ser				
1220		1225		1230
Gly Phe Gln Gly Glu Asp Thr Leu Leu Val Phe Val Tyr Lys Thr				
1235		1240		1245
Gly Lys Ser Tyr Ser Asp Phe Gly Gly Ser Asn Lys Asn Val Ala				
1250		1255		1260
Gly Met Thr Ile Tyr Gly Asp Gly Ser Phe Lys Lys Met Glu Asn				
1265		1270		1275
Thr Ala Leu Ser Arg Tyr Ser Gln Leu Lys Asn Thr Phe Asp Ile				
1280		1285		1290
Ile His Thr Gln Gly Asn Asp Leu Val Arg Lys Ala Ser Tyr Arg				
1295		1300		1305
Phe Ala Gln Asp Phe Glu Val Pro Ala Ser Leu Asn Met Gly Ser				
1310		1315		1320
Ala Ile Gly Asp Asp Ser Leu Thr Val Met Glu Asn Gly Asn Ile				
1325		1330		1335
Pro Gln Ile Thr Ser Lys Tyr Ser Ser Asp Asn Leu Ala Ile Thr				
1340		1345		1350
Leu His Asn Ala Ala Phe Thr Val Arg Tyr Asp Gly Ser Gly Asn				
1355		1360		1365
Val Ile Arg Asn Lys Gln Ile Ser Ala Met Lys Leu Thr Gly Val				
1370		1375		1380

Asp Gly	Lys Ser Gln Tyr Gly	Asn Ala Phe Ile Ile	Ala Asn Thr
1385		1390	1395
Val Lys	His Tyr Gly Gly Tyr	Ser Asp Leu Gly Gly	Pro Ile Thr
1400		1405	1410
Val Tyr	Asn Lys Thr Lys Asn	Tyr Ile Ala Ser Val	Gln Gly His
1415		1420	1425
Leu Met	Asn Ala Asp Tyr Thr	Arg Arg Leu Ile Leu	Thr Pro Val
1430		1435	1440
Glu Asn	Asn Tyr Tyr Ala Arg	Leu Phe Glu Phe Pro	Phe Ser Pro
1445		1450	1455
Asn Thr	Ile Leu Asn Thr Val	Phe Thr Val Gly Ser	Asn Lys Thr
1460		1465	1470
Ser Asp	Phe Lys Lys Cys Ser	Tyr Ala Val Asp Gly	Asn Asn Ser
1475		1480	1485
Gln Gly	Phe Gln Ile Phe Ser	Ser Tyr Gln Ser Ser	Gly Trp Leu
1490		1495	1500
Asp Ile	Asp Thr Gly Ile Asn	Asn Thr Asp Ile Lys	Ile Thr Val
1505		1510	1515
Met Ala	Gly Ser Lys Thr His	Thr Phe Thr Ala Ser	Asp His Ile
1520		1525	1530
Ala Ser	Leu Pro Ala Asn Ser	Phe Asp Ala Met Pro	Tyr Thr Phe
1535		1540	1545
Lys Pro	Leu Glu Ile Asp Ala	Ser Ser Leu Ala Phe	Thr Asn Asn
1550		1555	1560
Ile Ala	Pro Leu Asp Ile Val	Phe Glu Thr Lys Ala	Lys Asp Gly
1565		1570	1575
Arg Val	Leu Gly Lys Ile Lys	Gln Thr Leu Ser Val	Lys Arg Val
1580		1585	1590
Asn Tyr	Asn Pro Glu Asp Ile	Leu Phe Leu Arg Glu	Thr His Ser
1595		1600	1605

Gly	Ala	Gln	Tyr	Met	Gln	Leu	Gly	Val	Tyr	Arg	Ile	Arg	Leu	Asn
1610						1615					1620			
Thr	Leu	Leu	Ala	Ser	Gln	Leu	Val	Ser	Arg	Ala	Asn	Thr	Gly	Ile
1625						1630					1635			
Asp	Thr	Ile	Leu	Thr	Met	Glu	Thr	Gln	Arg	Leu	Pro	Glu	Pro	Pro
1640						1645					1650			
Leu	Gly	Glu	Gly	Phe	Phe	Ala	Asn	Phe	Val	Leu	Pro	Lys	Tyr	Asp
1655						1660					1665			
Pro	Ala	Glu	His	Gly	Asp	Glu	Arg	Trp	Phe	Lys	Ile	His	Ile	Gly
1670						1675					1680			
Asn	Val	Gly	Gly	Asn	Thr	Gly	Arg	Gln	Pro	Tyr	Tyr	Ser	Gly	Met
1685						1690					1695			
Leu	Ser	Asp	Thr	Ser	Glu	Thr	Ser	Met	Thr	Leu	Phe	Val	Pro	Tyr
1700						1705					1710			
Ala	Glu	Gly	Tyr	Tyr	Met	His	Glu	Gly	Val	Arg	Leu	Gly	Val	Gly
1715						1720					1725			
Tyr	Gln	Lys	Ile	Thr	Tyr	Asp	Asn	Thr	Trp	Glu	Ser	Ala	Phe	Phe
1730						1735					1740			
Tyr	Phe	Asp	Glu	Thr	Lys	Gln	Gln	Phe	Val	Leu	Ile	Asn	Asp	Ala
1745						1750					1755			
Asp	His	Asp	Ser	Gly	Met	Thr	Gln	Gln	Gly	Ile	Val	Lys	Asn	Ile
1760						1765					1770			
Lys	Lys	Tyr	Lys	Gly	Phe	Leu	Asn	Val	Ser	Ile	Ala	Thr	Gly	Tyr
1775						1780					1785			
Ser	Ala	Pro	Met	Asp	Phe	Asn	Ser	Ala	Ser	Ala	Leu	Tyr	Tyr	Trp
1790						1795					1800			
Glu	Leu	Phe	Tyr	Tyr	Thr	Pro	Met	Met	Cys	Phe	Gln	Arg	Leu	Leu
1805						1810					1815			
Gln	Glu	Lys	Gln	Phe	Asp	Glu	Ala	Thr	Gln	Trp	Ile	Asn	Tyr	Val
1820						1825					1830			

Tyr Asn Pro Ala Gly Tyr Ile Val Asn Gly Glu Ile Ala Pro Trp
 1835 1840 1845
 Ile Trp Asn Cys Arg Pro Leu Glu Glu Thr Thr Ser Trp Asn Ala
 1850 1855 1860
 Asn Pro Leu Asp Ala Ile Asp Pro Asp Ala Val Ala Gln Asn Asp
 1865 1870 1875
 Pro Met His Tyr Lys Ile Ala Thr Phe Met Arg Leu Leu Asp Gln
 1880 1885 1890
 Leu Ile Leu Arg Gly Asp Met Ala Tyr Arg Glu Leu Thr Arg Asp
 1895 1900 1905
 Ala Leu Asn Glu Ala Lys Met Trp Tyr Val Arg Thr Leu Glu Leu
 1910 1915 1920
 Leu Gly Asp Glu Pro Glu Asp Tyr Gly Ser Gln Gln Trp Ala Ala
 1925 1930 1935
 Pro Ser Leu Ser Gly Ala Ala Ser Gln Thr Val Gln Ala Ala Tyr
 1940 1945 1950
 Gln Gln Asp Leu Thr Met Leu Gly Arg Gly Gly Val Ser Lys Asn
 1955 1960 1965
 Leu Arg Thr Ala Asn Ser Leu Val Gly Leu Phe Leu Pro Glu Tyr
 1970 1975 1980
 Asn Pro Ala Leu Thr Asp Tyr Trp Gln Thr Leu Arg Leu Arg Leu
 1985 1990 1995
 Phe Asn Leu Arg His Asn Leu Ser Ile Asp Gly Gln Pro Leu Ser
 2000 2005 2010
 Leu Ala Ile Tyr Ala Glu Pro Thr Asp Pro Lys Ala Leu Leu Thr
 2015 2020 2025
 Ser Met Val Gln Ala Ser Gln Gly Gly Ser Ala Val Leu Pro Gly
 2030 2035 2040
 Thr Leu Ser Leu Tyr Arg Phe Pro Val Met Leu Glu Arg Thr Arg

2045		2050		2055
Asn Leu Val Ala Gln Leu Thr Gln Phe Gly Thr Ser Leu Leu Ser				
2060		2065		2070
Met Ala Glu His Asp Asp Ala Asp Glu Leu Thr Thr Leu Leu Leu				
2075		2080		2085
Gln Gln Gly Met Glu Leu Ala Thr Gln Ser Ile Arg Ile Gln Gln				
2090		2095		2100
Arg Thr Val Asp Glu Val Asp Ala Asp Ile Ala Val Leu Ala Glu				
2105		2110		2115
Ser Arg Arg Ser Ala Gln Asn Arg Leu Glu Lys Tyr Gln Gln Leu				
2120		2125		2130
Tyr Asp Glu Asp Ile Asn His Gly Glu Gln Arg Ala Met Ser Leu				
2135		2140		2145
Leu Asp Ala Ala Ala Gly Gln Ser Leu Ala Gly Gln Val Leu Ser				
2150		2155		2160
Ile Ala Glu Gly Val Ala Asp Leu Val Pro Asn Val Phe Gly Leu				
2165		2170		2175
Ala Cys Gly Gly Ser Arg Trp Gly Ala Ala Leu Arg Ala Ser Ala				
2180		2185		2190
Ser Val Met Ser Leu Ser Ala Thr Ala Ser Gln Tyr Ser Ala Asp				
2195		2200		2205
Lys Ile Ser Arg Ser Glu Ala Tyr Arg Arg Arg Arg Gln Glu Trp				
2210		2215		2220
Glu Ile Gln Arg Asp Asn Ala Asp Gly Glu Val Lys Gln Met Asp				
2225		2230		2235
Ala Gln Leu Glu Ser Leu Lys Ile Arg Arg Glu Ala Ala Gln Met				
2240		2245		2250
Gln Val Glu Tyr Gln Glu Thr Gln Gln Ala His Thr Gln Ala Gln				
2255		2260		2265

Leu	Glu	Leu	Leu	Gln	Arg	Lys	Phe	Thr	Asn	Lys	Ala	Leu	Tyr	Ser
2270						2275					2280			
Trp	Met	Arg	Gly	Lys	Leu	Ser	Ala	Ile	Tyr	Tyr	Gln	Phe	Phe	Asp
2285						2290					2295			
Leu	Thr	Gln	Ser	Phe	Cys	Leu	Met	Ala	Gln	Glu	Ala	Leu	Arg	Arg
2300						2305					2310			
Glu	Leu	Thr	Asp	Asn	Gly	Val	Thr	Phe	Ile	Arg	Gly	Gly	Ala	Trp
2315						2320					2325			
Asn	Gly	Thr	Thr	Ala	Gly	Leu	Met	Ala	Gly	Glu	Thr	Leu	Leu	Leu
2330						2335					2340			
Asn	Leu	Ala	Glu	Met	Glu	Lys	Val	Trp	Leu	Glu	Arg	Asp	Glu	Arg
2345						2350					2355			
Ala	Leu	Glu	Val	Thr	Arg	Thr	Val	Ser	Leu	Ala	Gln	Phe	Tyr	Gln
2360						2365					2370			
Ala	Leu	Ser	Ser	Asp	Asn	Phe	Asn	Leu	Thr	Glu	Lys	Leu	Thr	Gln
2375						2380					2385			
Phe	Leu	Arg	Glu	Gly	Lys	Gly	Asn	Val	Gly	Ala	Ser	Gly	Asn	Glu
2390						2395					2400			
Leu	Lys	Leu	Ser	Asn	Arg	Gln	Ile	Glu	Ala	Ser	Val	Arg	Leu	Ser
2405						2410					2415			
Asp	Leu	Lys	Ile	Phe	Ser	Asp	Tyr	Pro	Glu	Ser	Leu	Gly	Asn	Thr
2420						2425					2430			
Arg	Gln	Leu	Lys	Gln	Val	Ser	Val	Thr	Leu	Pro	Ala	Leu	Val	Gly
2435						2440					2445			
Pro	Tyr	Glu	Asp	Ile	Arg	Ala	Val	Leu	Asn	Tyr	Gly	Gly	Ser	Ile
2450						2455					2460			
Val	Met	Pro	Arg	Gly	Cys	Ser	Ala	Ile	Ala	Leu	Ser	His	Gly	Val
2465						2470					2475			
Asn	Asp	Ser	Gly	Gln	Phe	Met	Leu	Asp	Phe	Asn	Asp	Ser	Arg	Tyr
2480						2485					2490			

Leu Pro Phe Glu Gly Ile Ser Val Asn Asp Ser Gly Ser Leu Thr
2495 2500 2505

Leu Ser Phe Pro Asp Ala Thr Asp Arg Gln Lys Ala Leu Leu Glu
2510 2515 2520

Ser Leu Ser Asp Ile Ile Leu His Ile Arg Tyr Thr Ile Arg Ser
2525 2530 2535